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EXHIBIT A

A Polymorphism in the Protease-Like Domain of Apolipoprotein(a) Is Associated With Severe Coronary Artery Disease

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Objectives—The purpose of this study was to identify genetic variants associated with severe coronary artery disease (CAD).

Methods and Results—We used 3 case-control studies of white subjects whose severity of CAD was assessed by angiography. The first 2 studies were used to generate hypotheses that were then tested in the third study. We tested 12 077 putative functional single nucleotide polymorphisms (SNPs) in Study 1 (781 cases, 603 controls) and identified 302 SNPs nominally associated with severe CAD. Testing these 302 SNPs in Study 2 (471 cases, 298 controls), we found 5 (in *LPA*, *CALM1*, *HAP1*, *AP3B1*, and *ABCG2*) were nominally associated with severe CAD and had the same risk alleles in both studies. We then tested these 5 SNPs in Study 3 (554 cases, 373 controls). We found 1 SNP that was associated with severe CAD: *LPA* I4399M (rs3798220). *LPA* encodes apolipoprotein(a), a component of lipoprotein(a). I4399M is located in the protease-like domain of apolipoprotein(a). Compared with noncarriers, carriers of the 4399M risk allele (2.7% of controls) had an adjusted odds ratio for severe CAD of 3.14 (confidence interval 1.51 to 6.56), and had 5-fold higher median plasma lipoprotein(a) levels ($P=0.003$).

Conclusions—The *LPA* I4399M SNP is associated with severe CAD and plasma lipoprotein(a) levels. (***Arterioscler Thromb Vasc Biol.* 2007;27:2030-2036.**)

Key Words: coronary arteriosclerosis ■ genetics ■ single nucleotide polymorphism ■ lipoprotein(a) ■ risk factors

Severe coronary artery disease (CAD), characterized by occlusive epicardial coronary stenosis, and its consequences such as myocardial infarction (MI) are the leading causes of death in the United States.[1] Several major risk factors for coronary disease are well established and form the basis of current risk assessment algorithms.[2,3] However, some risk factors for coronary disease have not yet been identified, because some of the patients with coronary disease do not have traditional risk factors,[4] and traditional risk factors do not reliably predict premature MI.[5] The unidentified risk factors probably include genetic variants because genetics is considered to have an important role in coronary disease,[6,7] and a family history of cardiovascular disease is an independent risk factor.[8] One approach to identify genetic variants associated with complex diseases, such as coronary disease, is to use multiple association studies. We have previously identified genetic variants associated with MI and early-onset MI by testing thousands of putative functional SNPs in 3 case-control studies.[7,9] Thus, we have taken the same approach for angiographically defined severe CAD in 3 case-control studies, and asked if we could identify genetic variants associated with severe CAD.

Methods

Study Design

Because testing 12 077 SNPs for association with severe CAD could result in false-positives, we used 3 consecutive case-control studies. We generated a limited number of hypotheses in the first 2 studies by identifying a subset of SNPs that were nominally associated with severe CAD and had the same risk alleles in both studies and then tested these hypotheses in a third study.

Angiographic Assessment of CAD Severity

The severity of CAD was assessed by scoring the angiograms of subjects who had undergone clinically indicated coronary angiogra-

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TABLE 1. Clinical Characteristics of Cases and Controls in Study 1, Study 2, and Study 3

	Study 1			Study 2			Study 3		
Characteristic	Cases (n 781)	Controls (n=603)	*P* Value	Cases (n=471)	Controls (n=298)	*P* Value	Cases (n=554)	Controls (n 373)	*P* Value
Stenosis score*	270 (200–350)	0	N/A	355 (303–434)	0 (0–35)	N/A	300 (250–375)	0	N/A
Age, years	60±8	59±11	N/A	61±11	58±12	N/A	63±8	61±9	N/A
Male sex	480 (61)	376 (62)	N/A	252 (54)	166 (56)	N/A	358 (65)	164 (44)	N/A
Smoking†	531 (68)	326 (54)	<0.001	300 (64)	156 (52)	0.002	365 (66)	189 (51)	<0.001
Diabetes‡	286 (37)	63 (10)	<0.001	100 (21)	19 (6)	<0.001	230 (42)	54 (14)	<0.001
Hypertension‡	735 (94)	469 (78)	<0.001	297 (63)	135 (45)	<0.001	524 (95)	310 (83)	<0.001
Dyslipidemia‡	733 (95)	344 (59)	<0.001	411 (87)	183 (62)	<0.001	512 (94)	253 (70)	<0.001
BMI, kg/m^2	31±6	30±7	<0.001	28±5	27±5	0.06	30±6	30±7	0.48

Data presented as median (interquartile range) for stenosis score, mean±standard deviation for Age and BMI, or No. (%) of subjects for the other characteristics. N/A indicates that *P* values were not calculated because the characteristic was considered during the selection of cases and controls. *P* values are from Fisher exact test, except those for BMI, which are from the Wilcoxon rank sum test. BMI indicates body mass index.

*Calculation of the stenosis score is presented in supplemental Methods.

†Current or past smoking.

‡Subjects were considered to have this risk factor if the questionnaire indicated medical treatment for or a history of this risk factor.

phy. The severity of CAD was defined by a stenosis score calculated as the sum of the maximum percent stenosis in 10 coronary artery segments: the left main and 3 segments (proximal, medial, distal), each of the left anterior descending, left circumflex, and right coronary arteries. Details of the angiographic assessment of CAD and scoring methods used in these studies are described in the supplemental Methods (available online at http://atvb.ahajournals.org).

Study Subjects

Subjects in all 3 studies were unrelated women and men who had undergone coronary angiography (characteristics of cases and controls are presented in Table 1). Three goals of our study design influenced the choice of the stenosis score limits and the age limits used to select cases and controls. The first goal was to compare cases and controls at the extreme ends of the stenosis phenotype; the second goal was to include a large number of subjects; and the third goal was to select case and control groups that were about 40% or more female. Because males generally have higher stenosis score than females and have severe CAD at younger ages than females, we set stenosis score limits and age limits separately for males and females. Details of inclusion and exclusion criteria as well as stenosis score limits and age limits are described in supplemental Methods.

Subjects in Study 1 and Study 3 were drawn from the Cleveland Clinic Foundation (CCF) Genebank and included only those who selected Eastern European, Northern European, or "Caucasian Other" as the ethnicity for both parents. Study 1 comprised 781 cases and 603 controls selected from angiography patients enrolled in the CCF Genebank between December 2000 and March 2003 and whose DNA samples arrived at Celera before October 2003. Study 3 comprised 554 cases and 373 controls enrolled in the CCF Genebank between July 2001 and December 2003 and whose DNA samples arrived at Celera after August 2004. Subjects in Study 2 were drawn from Genomic Resource at University of California San Francisco (UCSF) and included those who selected only white as their ethnicity. Study 2 comprised 471 cases and 298 controls drawn from angiography patients enrolled between June 1990 and March 2003.

An additional group of 485 subjects who were not in Study 1, Study 2, or Study 3 were used to investigate the association between genotype and Lp(a) levels. These subjects had Lp(a) levels available in the database of the UCSF Genomic Resource and were drawn from the subjects of a previously published genetic study of MI.[9] The clinical characteristics of these 485 subjects are presented in supplemental Table I. Most of the Study 1 subjects (444 cases with a history of MI and 602 controls) and more than half (486 of 769) of Study 2 subjects, but none of the Study 3 subjects, were also subjects in the previously published genetic study of MI.[9]

All subjects gave informed consent and completed an Institutional Review Board approved questionnaire.

SNPs Tested

We tested 12 077 SNPs in Study 1. These putative functional SNPs are in 7439 genes, and 70% of the SNPs modify the amino acid sequence of the encoded proteins; the rest are potential regulatory SNPs (3′or 5′ untranslated regions, transcription factor binding sites, or exon splice sites). Additional SNPs in the LPA gene were selected using Tagger[10] as implemented in Haploview.[11]

Genotyping and Laboratory Measurements

Genotypes for individual DNA samples were determined by real-time kinetic polymerase chain reaction (PCR) as described previously.[9] Allele frequencies of SNPs were determined in Study 1 and Study 2 using pooled DNA samples as previously described.[9] The plasma Lp(a) levels in units of nmol/l. were determined by an ELISA method as previously described.[12] The size of apo(a) isoforms, reported as the number of KIV repeats in apo(a), was determined by immunoblotting as previously described.[13] Further details of these methods are described in supplemental Methods.

Statistical Analysis

Subject characteristics were summarized by disease status for each study, and differences were assessed using Fisher exact test or the Wilcoxon rank sum test for discrete and continuous characteristics, respectively. A chi-square test was used to assess allele frequency differences that were based on data from pooled DNA samples, and Fisher exact test was used to assess allele frequency differences that were based on genotyping results. An exact test was used to assess deviation of genotype frequencies from Hardy-Weinberg expectations.[14] When logistic regression was used to estimate odds ratios, significance was assessed using the Wald test. When risk alleles for severe CAD were prespecified based on Study 1 results for SNPs, the association of risk alleles with severe CAD was assessed in subsequent studies using 1-sided probability values and 90% confidence intervals (because there was 95% confidence that the true risk estimates were greater than the lower bounds of the 90% confidence intervals). All other probability values are 2-sided and 95% confidence intervals are presented. Likelihood ratio tests were used to evaluate potential interactions between genotype and each traditional risk factor in separate regression models that included an interaction term between genotype and the covariate of interest. The association

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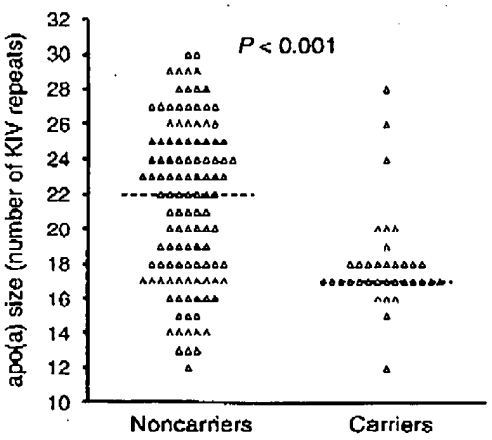

Figure 1. Association of the *LPA* I4399M SNP with apo(a) isoform size. Plasma apo(a) isoform sizes were determined for 114 noncarriers and 35 carriers of *LPA* I399M in Study 2. Carriers of the 4399M risk allele had significantly smaller apo(a) isoforms. Individual apo(a) isoform sizes (indicated by Δ) are reported as the number of KIV repeats in the apo(a) isoform, and the median sizes are indicated by the dashed lines.

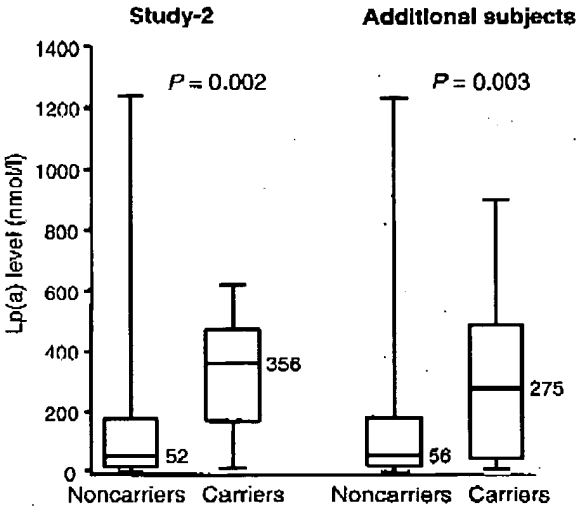

Figure 2. Association of the *LPA* I4399M SNP with plasma Lp(a) levels. In 161 Study 2 subjects for whom plasma Lp(a) levels were available, carriers of the *LPA* 4399M allele (n=12) had higher Lp(a) levels than did noncarriers (n=149). In an additional 485 subjects for whom plasma Lp(a) levels were available, carriers of the *LPA* 4399M allele (n=21) also had higher Lp(a) levels than did noncarriers (n=464). The median values are shown next to the boxes and indicated by the horizontal lines inside the boxes. The boxes extend from the 25th to 75th percentile and the whiskers extend from the lowest to the highest value.

of LPA I4399M genotype with apo(a) isoform size (Figure 1) and untransformed Lp(a) plasma levels (Figure 2) were assessed with the Wilcoxon rank sum test. A multiple linear regression model was used to estimate the relationship between the *LPA* I4399M carrier status and the ln of Lp(a) plasma levels while adjusting for the effect of apo(a) isoform size. The ln transformed Lp(a) levels were used in the linear regression analysis so that the distribution of the residuals more closely approximated a Gaussian distribution.

Results

LPA I4399M Is Associated With Severe CAD

The demographic and clinical characteristics of the subjects of Study 1, Study 2 and Study 3 are summarized in Table 1.

We measured the allele frequencies of 12 077 putative functional SNPs in Study 1 cases and controls using pooled DNA samples and identified 302 SNPs that were nominally associated with severe CAD ($P<0.05$) and had odds ratios for severe CAD of greater than 1.3 and had minor allele frequency estimates that were greater than 2% (supplemental Table II). For these 302 SNPs, we determined allele frequencies in Study 2 cases and controls using pooled DNA samples and asked if the risk allele identified in Study 1 was also associated with severe CAD in Study 2. For SNPs that were associated with severe CAD and had the same risk alleles in both pooling studies, we then confirmed their allele frequencies by genotyping individual DNA samples from Study 1 and Study 2 subjects. We found that the risk alleles of 5 SNPs in 5 genes were nominally associated ($P<0.05$) with severe CAD in both studies (Table 2). The genes encoded apolipoprotein(a) (encoded by *LPA*), calmodulin 1 (*CALM1*), huntingtin-associated protein 1 (*HAP1*), adaptor-related protein complex 3, β-1 subunit (*AP3B1*), and ATP-binding cassette, subfamily G, member 2 (*ABCG2*). The genotype distributions of these 5 SNPs in the control groups of Study 1 and Study 2 did not deviate from Hardy-Weinberg equilibrium expectations ($P>0.05$).

After prespecifying the risk alleles based on Study 1 and Study 2 results, we tested the hypotheses that the risk alleles of these 5 SNPs would be associated with severe CAD in Study 3. We found that the risk allele of 1 of the 5 SNPs, I4399M (rs3798220) in the *LPA* gene, was associated ($P<0.05$) with severe CAD. The *LPA* gene encodes apolipoprotein(a) (apo(a)), which is a component of lipoprotein(a) (Lp(a)), and the I4399M SNP is located in the protease-like domain of apo(a). Carriers of the 4399M allele constituted 2.7% of controls and 5.2% of cases in Study 3. Compared with noncarriers, carriers of the 4399M risk allele had an odds ratio for severe CAD of 3.14 (CI 1.51 to 6.56, $P=0.005$, Table 3) after adjusting for traditional risk factors (age, sex, smoking, hypertension, diabetes, dyslipidemia, and body mass index [BMI]). This association remained significant ($P=0.026$) after Bonferroni[15] correction for testing 5 SNPs in Study 3. We observed no indication of an interaction between the I4399M genotype and age, sex, smoking, diabetes, dyslipidemia, or BMI in Study 3 ($P>0.11$), but we did observe an interaction between genotype and hypertension ($P=0.02$). However, when we tested for interaction between I4399M genotype and hypertension in Study 1 and Study 2 we did not observe significant interactions ($I^2=0.94$ and $P=0.78$, respectively).

Genetic Variants in Linkage Disequilibrium With *LPA* I4399M

We used 2 approaches to investigate whether the association of *LPA* I4399M with severe CAD could be due to linkage disequilibrium (LD) between I4399M and other variants in the *LPA* gene. In the first approach, we asked whether other SNPs in the *LPA* gene were associated with severe CAD and

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TABLE 2. Unadjusted Association of 5 SNPs With Severe CAD in Study 1 and Study 2

SNP ID	Gene Symbol	Chromosome	Study	Major Allele*	Minor Allele*	Type of SNP*	Case AF†	Control AF†	OR‡	CI	P Value§
rs3798220	*LPA*	6	1	A	G	I4399M	0.04	0.01	3.79	1.97–7.29	<0.001
			2	A	G		0.04	0.02	2.25	1.27–3.97	0.010
rs3814843	*CALM1*	14	1	T	G	3′UTR	0.05	0.03	1.66	1.11–2.49	0.012
			2	T	G		0.06	0.04	1.74	1.13–2.67	0.020
rs4796603	*HAP1*	17	1	A	T	T58S	0.83	0.79	1.34	1.10–1.63	0.004
			2	A	T		0.83	0.78	1.36	1.09–1.68	0.012
rs6453373	*AP3B1*	5	1	A	T	E585V	0.94	0.92	1.51	1.11–2.04	0.008
			2	A	T		0.93	0.90	1.50	1.09–2.05	0.022
rs2231137	*ABCG2*	4	1	G	A	V12M	0.97	0.95	1.60	1.08–2.37	0.020
			2	G	A		0.96	0.94	1.62	1.10–2.38	0.028

*The polymorphic nucleotides on the sense strands are shown. Major alleles are on the left, and the risk alleles are bolded.
†Allele frequency for the risk allele.
‡Allelic odds ratios for the risk allele.
§For Study 1, 2-sided *P* values and 95% confidence intervals are reported. For Study 2, where the risk alleles have been prespecified based on Study 1, 1-sided *P* values and 90% confidence intervals are reported.
3′UTR indicates 3′ untranslated region.

could explain the association of I4399M with severe CAD. The HapMap project reports 65 SNPs in the *LPA* gene that have allele frequencies >2% in the CEU population (Utah residents with ancestry from northern and western Europe, HapMap public release #21). We identified a set of 18 SNPs that tagged 50 of these 65 SNPs with an r^2 >0.80, 12 SNPs with an r^2 <0.8 but >0.5, and 3 SNPs with an r^2 <0.5. We then genotyped the subjects of Study 1 (the largest of the 3 studies) for these 18 SNPs and the I4399M SNP which tags only itself. Except for the I4399M SNP, none of these 18 additional tagging SNPs was associated with severe CAD after adjusting for traditional risk factors (supplemental Table III). In Study 1 the I4399M SNP is not in strong LD with any of the other 18 tagging SNPs (r^2 ≤0.1), and the HapMap project does not report LD for the LPA I4399M SNP because that position is not polymorphic in the 30 CEU trios (60 parents and 30 offspring) genotyped by the HapMap project.

We also investigated whether the association of the *LPA* I4399M SNP with severe CAD could be attributable to LD between I4399M and the repeat polymorphism in the LPA gene that encodes the kringle IV (KIV) repeat length variation. This variation determines apo(a) isoform size which has been previously shown to be associated with coronary disease.[17] Direct determination of KIV repeat length in the *LPA* gene requires nucleated cells which were not available for these studies.[18] However, the KIV repeat length can also be determined from the number of KIV repeats in the apo(a) isoforms present in stored plasma.[19] Because stored plasma was available for some of the Study 2 subjects, we calculated the number of subjects needed to have 80% power to detect an association between the I4399M SNP and apo(a) isoform size (supplemental Methods). We then determined apo(a) isoform size for 35 carriers and 114 noncarriers of 4399M among Study 2 subjects. We found that in this group of 149 subjects, the I4399M SNP genotype was associated with apo(a) isoform size: the median apo(a) isoform size in carriers contained 17 KIV repeats and in noncarriers, 22 KIV repeats (P<0.001, Figure 1). However, in this group of 149 subjects, the association of the *LPA* 4399M allele with severe CAD remained significant after adjusting for the apo(a) size (odds ratio=4.36, CI 1.53 to 12.4, P=0.006; supplemental Table IV). Thus, we found no evidence that the association between the *LPA* 4399M allele with CAD is explained by apo(a) size polymorphism.

Plausibility of the Association of *LPA* I4399M With Severe CAD

To investigate the biological plausibility of the association between the *LPA* I4399M SNP and severe CAD, we asked

TABLE 3. Association of *LPA* I4399M With Severe CAD in Study 3

			Unadjusted			Adjusted§		
Genotype	Case*	Control*	OR†	CI‡	P Value‡	OR†	CI‡	P Value‡
MM	1 (0.2)	0 (0.0)	...	...	...	...	...	...
IM	28 (5.1)	10 (2.7)	1.94	1.05–3.59	0.039	3.09	1.48–6.48	0.006
MM+IM	29 (5.2)	10 (2.7)	2.01	1.09–3.70	0.031	3.14	1.51–6.56	0.005
II	525 (94.8)	363 (97.3)	1.00	reference		1.00	Reference	

*Data presented as No. (%) of subjects.
†Odds ratios were estimated by logistic regression.
‡*P* values (Wald test) are 1-sided and 90% CI are presented because the risk allele was prespecified.
§Adjusted for age, sex, smoking, diabetes, dyslipidemia, hypertension, and BMI.

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whether the SNP was associated with plasma levels of Lp(a), which have been associated with coronary disease.[20] Plasma Lp(a) levels were available in the UCSF Genomic Resource database for 161 subjects of Study 2 (these 161 subjects included 122 of the subjects shown in Figure 1; plasma Lp(a) levels were not available for Study 1 or Study 3 subjects). In these 161 subjects of Study 2, we found that Lp(a) levels were higher in carriers of the 4399M allele than in noncarriers ($P=0.002$): median levels were 356 nmol/L and 52 nmol/L, respectively (Figure 2). To confirm this result, we tested the association of the I4399M SNP with Lp(a) levels in 485 additional subjects with available Lp(a) levels (characteristics of these subjects are presented in supplemental Table I). These 485 subjects had not been included in Study 1, Study 2, or Study 3. In these 485 additional subjects, we again found that the Lp(a) levels were higher in carriers of the 4399M allele than in noncarriers ($P=0.003$, Figure 2).

We also asked whether the association of I4399M with Lp(a) levels can be explained by the association of I4399M with apo(a) size. Of the 161 Study 2 subjects who had Lp(a) levels available (left panel of Figure 2), 122 also had apo(a) size information available from the analysis in Figure 1. In these 122 subjects, we found that Lp(a) levels were 5.9-fold higher in carriers of the 4399M allele than in noncarriers, corresponding to a 1.78-ln unit increase in Lp(a) levels ($P=0.002$; supplemental Table V), and after adjusting for apo(a) size, Lp(a) levels remained 3.7-fold higher in carriers than in noncarriers, corresponding to a 1.32-ln unit increase in Lp(a) levels ($P=0.013$; supplemental Table V).

Discussion

We found that a genetic variant of *LPA*, the I4399M SNP, is associated with severe CAD. Carriers of the 4399M risk allele constituted 2.7% of the control subjects and had an adjusted odds ratio for severe CAD of 3.14 (90% CI 1.51 to 6.56; Table 3). This association seems unlikely to be a false-positive finding because it remained significant after correcting for multiple testing.

The *LPA* gene encodes the apo(a) protein of the Lp(a) particle, and high plasma Lp(a) levels are considered an emerging lipid risk factor for cardiovascular disease.[3,21] The variability in plasma Lp(a) levels among individuals are largely determined by genetic variations at the *LPA* gene locus,[22] a fraction of that variability has been attributed to variation in apo(a) size[22,23] resulting from the KIV type-2 repeat polymorphism.[19] The apo(a) protein in apparently healthy European Caucasians has been previously reported to contain a median of 27 KIV repeats.[24] The somewhat lower number of KIV repeats we observed in noncarriers (22 repeats) may reflect the higher than normal risk status of the subjects of our studies: all underwent clinically indicated coronary angiography. A number of other polymorphisms in the kringle region and in the 5′ noncoding region have also been reported to be associated with Lp(a) levels.[23,25–30]

We did not find evidence that the association of *LPA* I4399M with severe CAD was attributable to other variants in the *LPA* gene. We investigated 18 additional SNPs in the *LPA* gene that tagged 50 of the 65 SNPs that have allele frequency >2% in the HapMap CEU population. These 18 SNPs included 2 SNPs, T3907P and L3866V (same as T3888P and L3847V in Chretien et al), which have recently been reported to be associated with Lp(a) levels.[30] We found that none of these 18 SNPs could explain the association of LPA I4399M SNP with severe CAD. We also found that the apo(a) isoform size did not explain the association of *LPA* I4399M SNP with severe CAD.

Although we tested 12 077 putative functional SNPs from more than 7000 genes, the one genetic variant that remained associated with severe CAD in all 3 studies was the I4399M SNP in *LPA*, a gene that has often been implicated in vascular disease.[21] Thus, the association of *LPA* I4399M with severe CAD is biologically plausible both because *LPA* is a candidate gene for cardiovascular disease and also because this SNP is associated with Lp(a) levels (Figure 2). Whether or how the isoleucine to methionine substitution directly affects Lp(a) levels or CAD risk is not known. It is interesting to note that in apolipoprotein A-I, the oxidation of methionine residues has been shown to alter the sites and rates of the proteolytic cleavage of apolipoprotein A-I.[31] Thus we could speculate that potential oxidation of the 4399 methionine residue could alter apo(a) and Lp(a) catabolism, eg, by altering proteolytic fragmentation of either free or LDL-bound apo(a),[32] hence altering Lp(a) levels. Alternatively, it has been suggested that Lp(a) plays a role in fibrinolysis[21] and that it may be a carrier for proinflammatory and oxidized phospholipids[33]; both of these roles could conceivably be affected by a methionine substitution and its potential oxidation in the protease-like domain of apo(a). It would therefore be interesting to investigate the potential role of the I4399M SNP in Lp(a) physiology either in vitro or in transgenic animal models that overexpress the 2 I4399M alleles. Nevertheless, given that determining the KIV repeat length in the *LPA* gene or the apo(a) size in plasma requires more specialized techniques and samples that may not be available, the association of I4399M with apo(a) size could provide an alternative approach for obtaining information related to KIV repeat length or apo(a) size.

Results in this report contain several attributes that are considered desirable for a genetic association study,[34] including biological rationale, rigorous phenotyping and genotyping, multiple large sample sets, correction of probability values for multiple testing, and physiologically meaningful supporting evidence. It is worth noting that the I4399M SNP, which we found to be associated with severe CAD as well as with Lp(a) levels, has a relatively low frequency of about 2% in the control group. This finding suggests the need for designing sequencing projects with adequate power to detect SNPs of similar frequency. However, possible limitations include the inability of coronary angiography to identify circumferential disease; thus the stenosis score may have underestimated the extent of CAD for some of the control subjects. In addition, in Study 2 we tested only those SNPs that had had an odds ratio for severe CAD of greater than 1.3 in Study 1. Furthermore, even for SNPs with a true OR of 1.3, we had 80% power to detect association with severe CAD in Study 1 only for SNPs with minor allele frequencies of 0.2 or higher. This combination of a power limitation for low frequency SNPs in Study 1 and the odds-ratio cutoff we used

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to advance SNPs from Study 1 to Study 2 could have lead to false-negative results. Our analyses of Lp(a) levels and apo(a) size were restricted to those limited to a subset of subjects that had Lp(a) levels in the database and our analyses of apo(a) sizes were restricted to a subset of those subjects for whom plasma samples were in storage, and not all of these subjects had Lp(a) levels available. Apo(a) size determined from stored plasma may not fully reflect the genetic variability of the KIV repeat length polymorphism because larger apo(a) isoforms are secreted into the plasma at lower levels.[35] However, we could not directly determine the KIV repeat length in the *LPA* gene because nucleated cells were required but were not available. Finally, these results were derived from case-control studies of white subjects; thus the association of the *LPA* I4399M SNP with severe CAD and Lp(a) levels should be investigated in other ethnic groups and in prospective population-based cohorts.

In conclusion, we found that the I4399M genetic variant of *LPA* is associated with severe CAD, and the association remained significant after adjusting for multiple testing. The plausibility of this association is supported by the association of I4399M with Lp(a) levels. Functional studies of the *LPA* 4399M variant could shed light on the role of Lp(a) in the pathophysiology of vascular disease.

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Disclosures

M.L., D.M.L., C.R., D.S., J.C., D.U.L., A.A., C.T., and J.D. are current or former employees of Celera. J.K. and M.M. received funding from the University of California Discovery Grant Program which is jointly funded by the University of California and the State of California with matching funds from Celera. S.E. had been a paid consultant of Celera.

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EXHIBIT B

Online Supplement

A Polymorphism in the Protease-like Domain of Apolipoprotein(a) is Associated with Severe Coronary Artery Disease

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LPA online supplement

Methods

Angiographic Assessment of CAD Severity

The presence of CAD was assessed by performing coronary angiography as clinically indicated with each vessel imaged in multiple views of obliquity, including standardized views. Lesion narrowing was estimated in reference to adjacent angiographically normal appearing segments by highly experienced cardiologists. Since the Cleveland Clinic Foundation Genebank (CCF) and the Genomic Resource at the University of California San Francisco (UCSF) had enrolled subjects independently, the procedures used for recording and scoring coronary stenosis in subjects enrolled by CCF (Study-1 and Study-3) differed from those used at UCSF (Study-2). For subjects in Study-1 and Study-3 drawn from the CCF Genebank, lesions of less than 50% stenosis were coded as "<50%" and were not included in the calculation of the stenosis score so that patients without any lesion of 50% or more stenosis would have stenosis scores of zero. For subjects in Study-2 drawn from the Genomic Resource at UCSF, the procedure for recording and scoring coronary stenosis differed from those used at CCF in two respects. First, the percent stenosis of lesions of 10% or greater stenosis were recorded; second, up to two lesions for each of the ten coronary segments were summed to provide the stenosis score for that segment. Because of these differences in the scoring procedures, the stenosis scores from CCF and UCSF are not directly comparable, and the stenosis score for the UCSF subjects would in general be higher than those for the CCF subjects. However, within each study, the stenosis scores were calculated using the same procedure for all subjects and therefore were comparable between cases and controls within each study.

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Study Subjects

Three goals of our study design influenced the choice of the stenosis score limits and the age limits used to select cases and controls. The first goal was to compare cases and controls at the extreme ends of the stenosis phenotype, the second goal was to include a large number of subjects, and the third goal was to select case and control groups that were about 40% or more female. Since males generally have higher stenosis score than females and have severe CAD at younger ages than females, we set stenosis score limits and in Study-1 also age limits separately for males and females.

Study-1 comprised 781 cases and 603 controls selected from angiography patients enrolled in the CCF Genebank between December 2000 and March 2003 whose DNA samples arrived at Celera prior to October 2003. Controls were patients with a stenosis score of zero. Since young controls could become cases later in life, we excluded from controls females younger than 42 and males younger than 37 years old, these age cutoffs resulted in a control group that was 38% females. Patients with a history of MI, stroke, aortic aneurysm, aortic dissection, or carotid disease were also excluded from the control group of Study-1. For female cases we included patients with stenosis score greater than 75. For males, we included patients with stenosis score greater than 150. Since genetics plays a diminished role in the disease of older individuals, we excluded females older than 75 and excluded males older than 66 from the case group of Study-1. These age and stenosis score cutoffs resulted in a case group that was 39% female.

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Study-3 comprised 554 cases and 373 controls enrolled in the CCF Genebank between July 2001 and December 2003 whose DNA samples arrived at Celera after August 2004. Controls had stenosis score of zero and were 46 or older. This age cutoff resulted in a control group that was 56% female. Patients with a history of MI, stroke, aortic aneurysm, aortic dissection, carotid disease, or other peripheral vascular disease were excluded from the control group of Study-3. Female cases had stenosis score of 100 or higher, male cases had stenosis score of 250 of higher. These stenosis score cutoffs resulted in a case group that was 35% female.

Study-2 comprised 471 cases and 298 controls drawn from angiography patients enrolled between June 1990 and March 2003 in the Genomic Resource at UCSF. Since the stenosis score of Study-2 subjects would in general be higher than those of Study-1 and Study-3 subjects due to the different scoring procedure, female controls had stenosis score of 40 or lower and male controls had stenosis score of 100 or lower. These stenosis score cutoffs resulted in a control group that was 44% female. Patients with a history of MI, stroke, or aortic aneurysm were excluded from the control group of Study-2. Female cases had stenosis score of 200 or higher and male cases had stenosis score of 300 or higher. These stenosis score cutoffs resulted in a case group that was 46% female.

Genotyping and Laboratory Measurements

Genotypes for individual DNA samples were determined by real-time PCR as described previously.[1,2] Primer sequences and cycling conditions are available from the authors upon request. To assess genotyping accuracy, we also determined the genotype of the

LPA I4399M SNP for 2,906 subjects using an oligonucleotide ligation assay[3] and found > 99.9% concordance between the two methods, which is similar to what we had observed in previously published studies that compared these two genotyping methods.[1] Allele frequencies of SNPs were determined in Study-1 and Study-2 using DNA pools as previously described.[1,4] Briefly, each pool typically included 50 cases or controls and was made by mixing equal amounts of DNA from each individual member of the pool. Each allele was amplified separately by PCR using pooled DNA samples. The allele frequency for each pool was calculated from amplification curves for each allele. The plasma Lp(a) levels in units of nmol/l were determined by an ELISA method as previously described.[5]

The size of apo(a) isoforms, reported as the number of KIV repeats in apo(a), was determined by immunoblotting as previously described.[6] We attempted to determine the apo(a) isoform size for 155 subjects of Study-2 (39 carriers, 116 noncarriers), and succeeded for 149 subjects (35 carriers, 114 noncarriers). Of the 149, 101 had a single band and 48 had double bands. The mean isoform sizes were used where two isoforms were of equal intensity (6 of the 48 subjects with two bands), otherwise the sizes of the single or of the isoform present in higher level were used (the remaining 143 subjects).

Statistical Analysis

To determine sample size required to provide >80% power to detect an association of apo(a) size variation with the LPA I4399M genotype, we estimated from a previous report[7] the standard deviation in apo(a) size variation to be approximately 5 KIV repeats.

Using a more conservative assumption for a standard deviation of 7 KIV repeats, we calculated that a sample size of 50 carriers and 100 noncarriers would provide 90% power to detect differences in mean apo(a) size of 4 or more KIV repeats.

TABLE I (online). Clinical Characteristics of 485 Additional Subjects Enrolled by the UCSF Genomic Resource.

Characteristic	n=485
Age, yr	59 ± 10
Male sex	273 (56)
Smoking*	233 (48)
Diabetes†	38 (8)
Hypertension†	163 (34)
Dyslipidemia†	356 (73)
BMI, kg/m^2	27 ± 5

Data presented as number of subjects (%) or mean ± standard deviation.

*Current or past smoking.

†Subjects were considered to have this risk factor if the questionnaire indicated medical treatment for or a history of this risk factor.

TABLE II (online). 302 SNPs Nominally Associated with Severe CAD in Study-1

SNP	Gene	*P* value	SNP	Gene	*P* value
rs2231137	ABCG2	0.0004	rs2027937	CCHCR1	0.0257
rs11650404	ACCN1	0.0091	rs170360	CCL22	0.0156
rs1799805	ACHE	0.0181	rs17744917	CDH13	0.0011
rs12626485	ADAMTS5	0.0144	rs3740909	CDON	0.0090
rs3753494	AGL	0.0001	rs6692219	CEP350	0.0218
rs6964587	AKAP9	0.0001	rs881118	CHGB	0.0158
Chr10: 4862930	AKR1C1	0.0109	rs2231546	CHRNA10	0.0198
rs3809976	ALPK2	0.0002	rs2472553	CHRNA2	0.0031
rs11086065	ANKRD41	0.0046	rs3751334	CLDN10	0.0057
rs6896	ANXA7	0.0020	rs35822882	CLIC5	0.0301
rs6453373	AP3B1	0.0232	rs5247	CMA1	0.0178
Chr22: 34867709	APOL3	0.0148	Chr6: 25216902	CMAH	0.0407
rs35497285	ARHGEF10L	0.0197	Chr8: 87825071	CNGB3	0.0147
Chr11: 13335033	ARNTL	0.0198	Chr5: 179855171	CNOT6	0.0428
Chr9: 139627301	ARRDC1	0.0343	rs34165507	CNTNAP5	0.0350
rs2271589	ART5	0.0131	rs36117715	COL6A3	0.0188
rs1127767	ASB3	0.0029	rs12722877	COL9A2	0.0219
rs3886999	ATRN	0.0101	rs17258982	CR2	0.0456
rs34137317	BAT2	0.0002	rs35988674	CREB3L2	0.0360
rs1046080	BAT2	0.0024	rs36069724	CRISP2	0.0159
rs1044140	BAZ1A	0.0139	rs1048152	CSN3	0.0324
rs2484	BDH1	0.0286	rs2228603	CSPG3	0.0474
rs1046248	BDKRB2	0.0184	rs2916484	CTNNA2	0.0436
rs2071571	BRD2	0.0183	rs1925574	CTNNA3	0.0022
rs1558781	BTBD11	0.0330	rs10509681	CYP2C8	0.0084
rs35034250	BTD	0.0174	rs1675225	DCC	0.0248
rs28362681	BTNL2	0.0499	rs12022378	DCLRE1B	0.0002
rs7724813	BTNL8	0.0031	Chr8: 145513183	DGAT1	0.0151
Chr17: 75970089	C17orf27	0.0473	rs11653658	DHX33	0.0176
rs2304103	C19orf40	0.0439	rs2694558	DHX34	0.0197
rs12146709	C1QDC1	<0.0001	rs11734372	DKFZP686A01247	0.0002
rs9610624	C22orf33	0.0241	rs1537232	DNAH8	0.0173
rs36021078	C2orf13	0.0142	rs930571	DNAHL1	0.0048
Chr12: 8103051	C3AR1	0.0465	rs11550299	DPP3	0.0037
rs2076185	C6orf105	0.0264	rs267746	DUSP27	0.0143
Chr6: 88182261	C6orf165	0.0247	rs34075341	EDG3	0.0367
rs4076794	C9orf79	0.0088	rs11569017	EGF	0.0385
rs3814843	CALM1	0.0245	rs2480683	ELAVL4	0.0042
rs9812	CAMK2D	0.0003	rs6967117	EPHA1	0.0269
rs2107172	CAMK2D	0.0009	rs4653328	EPHA10	0.0015
rs1042636	CASR	0.0218	rs34364159	ETV6	0.0338
rs1801726	CASR	0.0092	rs1051881	EXOSC9	0.0061
rs472498	CCDC76	0.0044	rs11588069	FABP3	0.0105

SNP	Gene	*P* value	SNP	Gene	*P* value
rs2966952	FASTKD3	0.0155	rs2241913	LMO7	0.0060
rs3125818	FBXO6	0.0153	rs3885951	LOC123688	0.0083
rs1713480	FLJ11151	0.0078	rs11209235	LOC149224	0.0097
rs1995319	FLJ16686	0.0360	rs6026333	LOC149773	0.0096
Chr4: 36017150	FLJ16686	0.0282	Chr3: 186283788	LOC285382	0.0334
rs2287541	FLJ22662	0.0375	Chr14: 103629586	LOC374569	0.0296
rs8014119	FLJ38964	0.0038	rs17108179	LOC389997	0.0002
rs12999160	FLJ44048	0.0186	rs12741980	LOC390997	0.0073
rs1379074	FMN2	0.0024	rs943133	LOC391102	0.0005
rs17553619	FNDC7	0.0118	rs2832129	LOC391276	0.0026
rs16932300	FREM1	0.0295	Chr2: 63833162	LOC391378	0.0191
rs3025628	GABBR1	0.0456	rs1691283	LOC440585	0.0068
rs11681174	GALNT14	0.0135	rs6005327	LOC440799	0.0002
rs2578652	GANC	0.0084	rs17436236	LOC442660	0.0383
rs699664	GGCX	0.0003	rs2457151	LOC646616	0.0006
rs35951334	GLI3	0.0410	rs34882755	LOC646643	0.0229
rs2297775	GON4L	0.0005	rs17841161	LOC727963	0.0167
rs3741822	GPRC5D	0.0269	Chr8: 109064944	LOC728381	0.0190
rs34637004	GRHL3	0.0368	rs388288	LOC729745	0.0041
rs2607861	GRID1	0.0347	rs3798220	LPA	<0.0001
rs3808117	GRM8	0.0002	rs1546417	LRBA	0.0021
rs868733	H2AFY	0.0143	rs3745974	LRP3	0.0076
rs4796603	HAP1	0.0003	Chr4: 3496440	LRPAP1	0.0271
rs1126472	HIVEP1	0.0118	rs35932273	LTK	0.0167
rs10901322	HMCN2	0.0006	rs10923322	MAN1A2	0.0007
rs11881940	HNRPUL1	0.0005	rs17745550	MAP2	0.0082
rs3745297	HRC	0.0005	Chr18: 72857811	MBP	0.0467
rs11539471	HSD17B4	0.0025	rs937652	MCCC1	0.0044
rs1176739	HTR3B	0.0295	rs7905784	MCM10	0.0017
rs2901127	IFIR7	0.0322	rs17152897	MCM10	0.0321
rs12487205	IGSF10	0.0288	rs236110	MCM8	0.0259
rs763780	IL17F	0.0122	rs930557	MCPH1	0.0007
rs988574	ITGA1	0.0068	rs4707569	MDN1	0.0078
rs2229006	KCNB1	0.0208	rs429433	MFHAS1	0.0302
rs34989303	KCNK6	0.0084	rs33993717	MGC11332	0.0111
rs13218075	KIAA0319	0.0008	rs17258507	MGC4562	0.0372
rs3742591	KIAA0423	0.0250	Chr12: 31706434	MGC50559	0.0200
rs3751336	KIAA0774	0.0380	rs11593531	MGMT	0.0323
Chr16: 52277937	KIAA1005	0.0391	rs3825549	MIA2	0.0205
rs17578364	KIAA1107	0.0002	rs2131025	MITF	0.0139
rs12296548	KRT76	0.0200	rs6010260	MLC1	0.0219
rs34536322	LACTB	0.0108	rs2997211	MPP7	0.0122
Chr15: 98886566	LASS3	0.0160	rs184967	MSH3	0.0079
Chr10: 90564937	LIPL3	0.0407	Chr6: 37045618	MTCH1	0.0057
rs11578818	LMO4	0.0074	rs17854374	MTDH	0.0059

SNP	Gene	*P* value	SNP	Gene	*P* value
rs2946655	MTFMT	0.0254	rs12700364	RAPGEF5	0.0174
rs28383653	MTNR1A	0.0018	rs34141181	RLF	0.0029
rs2306985	MTTP	0.0002	rs619203	ROS1	0.0001
Chr4: 100723589	MTTP	0.0030	rs529038	ROS1	0.0003
rs17467284	MUC19	0.0285	rs2273373	RP5-1022P6.2	0.0367
rs2791718	MYBPH	0.0297	rs3133187	RPS3	0.0276
rs589855	NAV1	0.0116	rs35224605	RTP4	0.0117
rs1818	NCOA6IP	0.0172	rs35364374	RYR1	0.0346
rs165602	NEFH	0.0091	rs34297715	SCARF1	0.0279
rs12684749	NFIB	0.0017	rs34627298	SDAD1	0.0132
rs2236316	NIN	0.0020	rs17260829	SERINC1	0.0137
rs34248917	NPHP4	0.0001	rs2289519	SERPINB5	0.0053
rs2289657	NTRK2	<0.0001	rs34687326	SLAMF8	0.0170
rs2279685	NUT	0.0190	rs2297322	SLC15A1	0.0013
rs2487999	OBFC1	0.0264	rs1171614	SLC16A9	0.0010
rs34883368	OGFOD1	0.0022	rs2073714	SLC22A14	0.0109
rs13294411	OR13D1	0.0430	rs12520516	SLC36A3	0.0243
rs16895070	OR2I1P	0.0304	rs35690712	SLC39A7	0.0272
rs9905086	OR3A4	0.0153	Chr15: 90252909	SLCO3A1	0.0225
rs12420187	OR52J2P	0.0008	rs6968199	SND1	0.0002
rs16906358	OR52M2P	0.0456	rs3757767	SND1	0.0113
Chr11: 56165586	OR5AP2	0.0280	rs799489	SRP54	0.0010
rs2217657	OR7G1	<0.0001	rs33952588	STX18	0.0071
rs2195951	OR7G1	0.0074	rs235293	SUMO3	0.0145
rs12788990	OR8U1	0.0023	rs872665	SVEP1	0.0017
rs2272629	PADI3	0.0318	rs3820594	SYT11	0.0011
rs3750300	PADI3	0.0490	rs619381	TAS2R7	0.0080
rs9581043	PARP4	0.0395	rs4964460	TCP11L2	0.0005
rs712701	PAX4	0.0019	rs4468717	TGIF	0.0081
rs3776096	PCDHB6	0.0024	rs2285744	THSD7A	0.0006
rs12407957	PDC	0.0033	rs34848112	TIPIN	0.0181
rs11598673	PDCD11	0.0054	rs2286025	TMEM106C	0.0354
rs1049306	PDHX	0.0178	rs2155587	TMEM123	0.0384
Chr7: 10989085	PHF14	0.0134	rs1436213	TMEM23	0.0009
rs2880205	PHKB	0.0430	rs3740997	TRIM34	0.0299
rs3862712	PIGN	0.0115	rs11038628	TRIM5	0.0134
rs12825178	PIK3C2G	0.0037	rs1339847	TRIM58	0.0044
rs17508082	PLCE1	0.0464	rs9899862	TTYH2	0.0007
rs2076213	PNPLA3	0.0376	rs12206717	TULP4	0.0418
rs11243406	POMT1	0.0349	rs34585936	UNC5C	0.0392
rs3734729	PPP1R14C	0.0361	rs1323717	USP45	0.0153
rs34473884	PPP2R2D	0.0032	rs1010	VAMP8	0.0001
rs11657445	PRKAR1A	0.0067	rs10507051	VEZT	0.0137
rs2824804	PRSS7	0.0389	rs1800391	WRN	0.0062
rs4603	PSMB4	0.0003	rs7310136	YARS2	0.0135

SNP	Gene	*P* value	SNP	Gene	*P* value
Chr5: 112948007	YTHDC2	0.0069	rs6900025	–*	0.0185
rs2236424	ZC3HAV1	0.0102	Chr15: 92518418	–*	0.0340
rs11993776	ZFPM2	0.0254	rs28626499	–*	0.0012
rs35625154	ZNF175	0.0182	Chr14: 19977112	–*	0.0386
rs2068061	ZNF224	0.0068	rs4866054	–*	0.0309
rs2393938	ZNF239	0.0146	Chr21: 34694847	–*	0.0139
rs12611425	ZNF254	0.0322	Chr11: 56153361	–*	0.0462
rs926487	ZNF337	0.0007	Chr4: 106416449	–*	0.0191
rs2278415	ZNF350	0.0059	rs12549649	–*	0.0022
rs36083942	ZNF508	0.0098			
rs2232647	ZNF593	0.0258			
rs3764537	ZNF614	0.0164			
rs7254529	ZNF763	0.0251			
rs2560876	ZNF766	0.0218			
Chr11: 55279315	–*	0.0441			
Chr11: 55279356	–*	0.0060			
rs1992149	–*	0.0174			
rs585063	–*	0.0296			
rs2875428	–*	0.0352			
rs1026463	–*	<0.0001			
Chr6:171070390†	–*	0.0051			
Chr5: 119044452	–*	0.0096			
Chr3: 143245489	–*	0.0131			
rs297177	–*	0.0004			
rs718720	–*	0.0064			
rs593772	–*	0.0351			
rs1052895	–*	0.0013			

All the rs numbers, chromosome locations, and gene symbols are from NCBI build 36 unless noted otherwise.

*Not annotated as a gene in NCBI Build 36.

†Position based on Celera genome assembly (R27).

TABLE III (online). Association of 18 Additional SNPs in the *LPA* gene with Severe CAD in Study-1

	Unadjusted		Adjusted‖			
SNP ID	OR*	*P* value†	OR*	*P* value†	Relative Position, bp‡	SNP Type§
rs3124784	1.01	0.893	1.05	0.642	0	R4524C
rs3127596	1.01	0.950	1.04	0.725	197	Tagging
Chr6:160873462	0.86	0.461	0.87	0.589	634	Tagging
rs6919346	0.76	0.007	0.84	0.188	7521	Tagging
rs3798220	**4.19**	**<.0001**	**2.91**	**0.007**	**8299**	**I4399M**
rs7767084	1.04	0.689	1.06	0.680	9665	Tagging
rs11751605	1.05	0.678	1.12	0.398	10392	Tagging
rs10755578	1.05	0.513	1.06	0.547	16900	Tagging
rs10945675	1.03	0.758	1.05	0.625	21590	Tagging
rs6415084	1.00	0.962	0.97	0.774	27492	Tagging
rs3798221	0.85	0.099	0.88	0.328	45310	Tagging
rs6939089	1.10	0.639	0.95	0.836	50998	Tagging
Chr6:160926162	1.17	0.167	1.12	0.415	53334	T3907P
rs7765803	0.98	0.778	0.98	0.886	54700	L3866V
rs7771801	0.98	0.831	0.99	0.941	55277	Tagging
rs9355296	1.03	0.817	0.98	0.871	65155	Tagging
rs35600881	0.87	0.148	0.84	0.160	73926	Tagging
rs13202636	0.87	0.136	0.85	0.160	76890	Tagging
rs6929299	0.99	0.918	0.98	0.836	79251	Tagging

*Odds ratio for each allele was estimated in a model that assumed risk was additive on the log scale.

†*P* values are from Wald test and are 2-sided.

‡Based on NCBI Genome Build 36.

§Tagging SNPs are designated based on HapMap[8] using Tagger as implemented in Haploview,[9] amino acid positions are based on a published protein sequence.[10]

‖Adjusted for age, sex, smoking, diabetes, dyslipidemia, hypertension, and BMI.

Bold type indicates the I4399M SNP.

T3907P and T3866V are the same as T3888P and L3847V in Chretien *et al.* [11], which counts from the first amino acid after the signal peptide.

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TABLE IV (online). Association of *LPA* I4399M and Apo(a) Size With Severe CAD

	Case*	Control*	Unadjusted OR	Unadjusted CI‡	Unadjusted *P* value‡	Adjusted§ OR	Adjusted§ CI‡	Adjusted§ *P* value‡
I4399M								
MM+IM	30	5	5.40	1.96 -14.9	0.001	4.36	1.53-12.4	0.006
II	60	54	1.00	reference		1.00	reference	
apo(a)†								
KIV	90	59	0.90	0.83-0.97	0.008	0.93	0.86-1.01	0.090

*Analysis of Study-2 cases and controls with apo(a) size information available, n = 149.

†The apo(a) size was coded as an ordinal variable corresponding to the number of KIV repeats, where the odds ratio for severe CAD for apo(a) was calculated to estimate the risk associated with each additional KIV repeat.

‡*P* values are two-sided and 95% CI are presented. *P* values were by Wald test.

§In the models that estimated adjusted odds ratios for severe CAD, the risk associated with 4399M was adjusted for apo(a) size, the number of KIV repeats, and the risk associated with apo(a) size was adjusted for 4399M carrier status.

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TABLE V (online). Association of *LPA* I4399M and Apo(a) Size With the Natural Log of Plasma Lp(a) Levels

Variable	coefficient	95% CI	*P* value
I4399M			
Intercept	3.93	3.64-4.22	<0.001
MM+IM	1.78	0.65-2.90	0.002
apo(a) size			
Intercept	7.45	6.22-8.68	<0.001
KIV repeats	-0.16	-0.22-(-0.10)	<0.001
I4399M and apo(a) size			
Intercept	7.11	5.88-8.35	<0.001
MM+IM	1.32	0.28-2.35	0.013
KIV repeats	-0.15	-0.21-(-0.09)	<0.001

Study-2 subjects with Lp(a) level and apo(a) size available, n = 122. The coefficients were estimated by linear regression. The coefficients indicate the change in the mean natural log of Lp(a) level per unit increase in the variable. The I4399M variable was coded 1 for carriers and 0 for noncarriers. The apo(a) size variable was the number of KIV repeats. *P* values were calculated with an F test.

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